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-43. In a method of synthesizing secondary metabolites in Sac. erythrae, the improvement comprising using at least one of the DNA sequence selected from the group consisting of sequences eryBII (complementary sequence of SEQ ID No: 1 from nucleotide 48 to nucleotide 1046), eryCIII (complementary sequence of SEQ ID No: 1 from nucleotide 1046 to nucleotide 2308) or eryCII (complementary sequence of SEQ ID No: 1 from nucleotide 2322 to nucleotide 3404) represented in Figure 2, eryBIV (sequence of SEQ ID No: 6 from nucleotide 242 to nucleotide 1207), eryBV (sequence of SEQ ID No: 6 from nucleotide 1210 to nucleotide 2454), eryCVI (sequence of SEQ ID No: 7 from nucleotide 2510 to nucleotide 3220), eryBVI (sequence of SEQ ID No: 6 from nucleotide 3308 to nucleotide 4837), eryCIV (sequence of SEQ ID No: 6 from nucleotide 4837 to nucleotide 6039), eryCV (sequence of SEQ ID No: 6 from nucleotide 6080 to nucleotide 7546), of eryBVII (sequence of SEQ ID No: 6 from nucleotide 7578 to nucleotide 8156) represented in Figure 3, to synthesize hybrid secondary metabolites in Sac. erythrae--

--44. In a method of using hybridization probes, the improvement comprising using as the hybridization probe at least one DNA sequence selected from the group consisting of eryBII (complementary sequence of SEQ ID No: 1 from nucleotide 48 to nucleotide 1046), eryCIII (complementary sequence of SEQ ID No: 1 from nucleotide 1046 to nucleotide 2308) or eryCII (complementary sequence of SEQ ID No: 1 from nucleotide 2322 to nucleotide 3404) represented in Figure 2, eryBIV (sequence of SEQ ID No: 6 from nucleotide 242 to nucleotide 1207), eryBV (sequence of SEQ ID No: